

SEQUENCE ALIGNMENT OF SEQ ID NO: 2 AND 4 AGAINST

HUMAN γ -HEREGULIN

RESULT 9

AAW44817

ID AAW44817 standard; Protein; 768 AA.

XX

AC AAW44817;

XX

DT 17-AUG-1998 (first entry)

XX

DE Human gamma-hereregulin.

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KW Gamma-hereregulin; gamma-HRG; human; autocrine growth factor;

KW breast cancer; MDA-MB-175 cell; diagnosis; gene therapy;

KW ErbB receptor; cell proliferation; cell differentiation;

KW cell survival; neurological disorder; muscular disorder.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT Domain 1..560

FT /note= "N-terminal domain (Claim 5)"

FT Region 342..363

FT /note= "hydrophobic region, may function as
internal signal sequence"

FT Domain 704..748

FT /note= "EGF-like domain"

FT Modified-site 77

FT /note= "N-glycosylated"

FT Modified-site 151

FT /note= "N-glycosylated"

FT Modified-site 467

FT /note= "N-glycosylated"

FT Modified-site 647

FT /note= "N-glycosylated"

FT Modified-site 653

FT /note= "N-glycosylated"

FT Modified-site 691

FT /note= "N-glycosylated"

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PN WO9802541-A1.

XX

PD 22-JAN-1998.

XX

PF 08-JUL-1997; 97WO-US11841.

XX

PR 12-JUL-1996; 96US-0021640.

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PA (GETH) GENENTECH INC.

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PI Schaefer GM, Sliwkowski M;

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DR WPI; 1998-110589/10.

DR N-PSDB; AAV19251.

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PT DNA encoding gamma-hereregulin - used to activate ErbB receptor and to

PT enhance proliferation, differentiation or survival of a cell

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PS Claim 3; Fig 1A-C; 81pp; English.

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CC This polypeptide comprises human gamma-hereregulin (gamma-HRG), a

CC novel member of the hereregulin superfamily, that has a unique

CC N-terminal domain not present in previously identified hereregulins.

CC Gamma-HRG is secreted by human breast cancer MDA-MB-175 cells. It

CC leads to the formation of a constitutive active receptor complex

CC and stimulates the growth of these cells in an autocrine manner.

CC A claimed method for activating an ErbB receptor comprises contact

CC a cell which expresses the receptor with gamma-HRG. A claimed

CC method for enhancing the proliferation, differentiation or survival

CC of a cell, especially a glial cell or muscle, comprises contacting

CC the cell with gamma-HRG. Antibodies raised against the unique

CC N-terminal domain of gamma-HRG can be used to detect and purify

CC the protein. Antagonists of gamma-HRG can be used to block

CC gamma-HRG activity and expression. The gamma-HRG may be obtained
CC from claimed host cells that comprise a vector containing an
CC isolated gamma HRG nucleic acid (see AAV19251).
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SQ Sequence 768 AA;

Query Match 20.3%; Score 3003; DB 19; Length 768;
Best Local Similarity 76.7%; Pred. No. 9.7e-161;
Matches 600; Conservative 22; Mismatches 82; Indels 78; Gaps 10;

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Qy 1 MDVKERKPYRSLTRRRDAERRYSSSSADSEEGKAPQKSYSSSETLKAYDQDARLAYGSRV 60
   |||
Db 1 MDVKERKPYRSLTRRRDAERRYSSSSADSEEGKAPQKSYSSSETLKAYDQDARLAYGSRV 60

Qy 61 KDIVPQEAEEFCRTGANFTLRELGLEEVTPPHGTLYRTDIGLPHCGYSMGAGSDADMEAD 120
   |||
Db 61 KDIVPQEAEEFCRTGANFTLRELGLEEVTPPHGTLYRTDIGLPHCGYSMGAGSDADMEAD 120

Qy 121 TVLSPEHPVRLWGRSTRSGRSSCLSSRANSNLTLTDEHENTETDHPGGLQNHARLRTPP 180
   |||
Db 121 TVLSPEHPVRLWGRSTRSGRSSCLSSRANSNLTLTDEHENTETDHPGGLQNHARLRTPP 180

Qy 181 PPLSHAHTPNQHHAASINSLNRGNFTPRSNPSPAPTDHSLSGEPPAGGAQEPAAHQENWL 240
   |||
Db 181 PPLSHAHTPNQHHAASINSLNRGNFTPRSNPSPAPTDHSLSGEPPAGGAQEPAAHQENWL 240

Qy 241 LNSNIPLERNLGKQPFGLTLDNLIEMDILGASRHDGAYS DGHFLFKPGGTSPLFCTTS 300
   |||
Db 241 LNSNIPLERNLGKQPFGLTLDNLIEMDILGASRHDGAYS DGHFLFKPGGTSPLFCTTS 300

Qy 301 PGYPLTSSTVYSPPPRPLRSTFARPAFNLKKPSKYCNWKAALSAIVISATLVILLAYF 360
   |||
Db 301 PGYPLTSSTVYSPPPRPLRSTFARPAFNLKKPSKYCNWKAALSAIVISATLVILLAYF 360

Qy 361 VAMHLFGLNWLQPMEGQMYEITEDTASSWPVPTDVS LYPSSGGTGLET PDRKGKGTEGK 420
   |||
Db 361 VAMHLFGLNWLQPMEGQMYEITEDTASSWPVPTDVS LYPSSGGTGLET PDRKGKGTEGK 420

Qy 421 PSSFFPEDSFIDSGEIDVGRRASQKIPPGTFWRSQVFI DHPVHLKFNVS LGAALVGIYG 480
   |||
Db 421 PSSFFPEDSFIDSGEIDVGRRASQKIPPGTFWRSQVFI DHPVHLKFNVS LGAALVGIYG 480

Qy 481 RKGLPPSHTQDFVELLDGRRLLTQEARSLEGT PRQSRGTVPSSHETGFIQYLD SGIWH 540
   |||
Db 481 RKGLPPSHTQDFVELLDGRRLLTQEARSLEGT PRQSRGTVPSSHETGFIQYLD SGIWH 540

Qy 541 LAFYNDGKESEVVSFLTTAI---ESVDNCP SNCYGN GD-----CISGTCHCFLGFL---- 588
   |||
Db 541 LAFYNDGKESEVVSFLTTAIALPPRLKEMKQESAAGSKLVLR CETSSEYSSLRFKWFKN 600

Qy 589 GPD CGRASC P-----VLC SGN GQYMKGRCLCHSGWKGAECDVPTNQ C 630
   | : | : | : : : | :
Db 601 GNELNRKNKPQNIKI QKKPGKSEL RINKASLADSGEYM-----CKVISKLG 646

Qy 631 IDVACSNHGTCTGTCTICNPGYKGESCEEVD CMDPTCSGRGV CVRGECHCSVWG GGTNCE 690
   || : || : || : || : || : ||
Db 647 NDSASAN---ITIV-----ESNEIITGMPASTEGAYVSSESP IRISVSTEGANTS 693

Qy 691 TPRAT-----CLDQ-----CSGHGTFL-----PDTGLCSCDPSWTHDCSIEIC 729
   : : | : : : : | : | : | :
Db 694 SSTSTSTGTSHLVKCAEKEKTF CVNGGECFMVKDLSNPSRYLCKCPNEFTGDRCQNYVM 753

Qy 730 AA 731
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Db 754 AS 755
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